

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BENOIT, Patrick  
MEYER, Francois  
MAGUIRE, Deborah  
PLAVEC, Ivan  
TOVEY, Michael G.
- (ii) TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
INTERFERON
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Foley & Lardner  
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(C) CITY: Washington  
(D) STATE: D.C.  
(E) ZIP: 20007
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/307,588  
(B) FILING DATE: 05-DEC-1994
- C' (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/EP93/00770  
(B) FILING DATE: 30-MAR-1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: EP 92400902.0  
(B) FILING DATE: 31-MAR-1992
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: SAXE, Bernhard D.  
(B) REGISTRATION NUMBER: 28,665  
(C) REFERENCE/DOCKET NUMBER: 17283/117/GUPL
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (202)672-5300  
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1343 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 27..1334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGCAGGGAT CTGCGGCGGC TCCCAG ATG ATG GTC GTC CTC CTG GGC GCG ACG	53
Met Met Val Val Leu Leu Gly Ala Thr	
1 5	
ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA	101
Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala	
10 15 20 25	
GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTA GAG GTC GAC ATC ATA	149
Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile	
30 35 40	
GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG	197
Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly	
45 50 55	
AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG	245
Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp	
60 65 70	
ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT	293
Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe	
75 80 85	
TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA	341
Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg	
90 95 100 105	
GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA	389
Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr	
110 115 120	
CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT	437
Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala	
125 130 135	
GAA GAT AAG GCA ATA GTG ATA CAC ATC TCT CCT GGA ACA AAA GAT AGT	485
Glu Asp Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser	
140 145 150	
GTT ATG TGG GCT TTG GAT GGT TTA AGC TTT ACA TAT AGC TTA CTT ATC	533
Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Leu Ile	
155 160 165	
TGG AAA AAC TCT TCA GGT GTA GAA GAA AGG ATT GAA AAT ATT TAT TCC	581
Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser	
170 175 180 185	
AGA CAT AAA ATT TAT AAA CTC TCA CCA GAG ACT ACT TAT TGT CTA AAA	629
Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys	
190 195 200	
GTT AAA GCA GCA CTA CTT ACG TCA TGG AAA ATT GGT GTC TAT AGT CCA	677
Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro	
205 210 215	
GTA CAT TGT ATA AAG ACC ACA GTT GAA AAT GAA CTA CCT CCA CCA GAA	725
Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu	
220 225 230	
AAT ATA GAA GTC AGT GTC CAA AAT CAG AAC TAT GTT CTT AAA TGG GAT	773
Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp	
235 240 245	

c' cont

TAT ACA TAT GCA AAC ATG ACC TTT CAA GTT CAG TGG CTC CAC GCC TTT 821  
 Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe  
 250 255 260 265  
 TTA AAA AGG AAT CCT GGA AAC CAT TTG TAT AAA TGG AAA CAA ATA CCT 869  
 Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro  
 270 275 280  
 GAC TGT GAA AAT GTC AAA ACT ACC CAG TGT GTC TTT CCT CAA AAC GTT 917  
 Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val  
 285 290 295  
 TTC CAA AAA GGA ATT TAC CTT CTC CGC GTA CAA GCA TCT GAT GGA AAT 965  
 Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly Asn  
 300 305 310  
 AAC ACA TCT TTT TGG TCT GAA GAG ATA AAG TTT GAT ACT GAA ATA CAA 1013  
 Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln  
 315 320 325  
 GCT TTC CTA CTT CCT CCA GTC TTT AAC ATT AGA TCC CTT AGT GAT TCA 1061  
 Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser  
 330 335 340 345  
 TTC CAT ATC TAT ATC GGT GCT CCA AAA CAG TCT GGA AAC ACG CCT GTG 1109  
 Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val  
 350 355 360  
 ATC CAG GAT TAT CCA CTG ATT TAT GAA ATT ATT TTT TGG GAA AAC ACT 1157  
 Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr  
 365 370 375  
 TCA AAT GCT GAG AGA AAA ATT ATC GAG AAA AAA ACT GAT GTT ACA GTT 1205  
 Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val  
 380 385 390  
 CCT AAT TTG AAA CCA CTG ACT GTA TAT TGT GTG AAA GCC AGA GCA CAC 1253  
 Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His  
 395 400 405  
 ACC ATG GAT GAA AAG CTG AAT AAA AGC AGT GTT TTT AGT GAC GCT GTA 1301  
 Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val  
 410 415 420 425  
 TGT GAG AAA ACA AAA CCA GGA AAT ACC TCT AAA TGAGGTACC 1343  
 Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys  
 430 435

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val  
 1 5 10 15  
 Gly Pro Trp Val Leu Ser Ala Ala Ala Gly Gly Lys Asn Leu Lys Ser  
 20 25 30

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg  
35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp  
50 55 60

Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln  
65 70 75 80

Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val  
85 90 95

Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser  
100 105 110

Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile  
115 120 125

Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp Lys Ala Ile Val Ile  
130 135 140

His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly  
145 150 155 160

Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val  
165 170 175

Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu  
180 185 190

Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr  
195 200 205

Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr  
210 215 220

Val Glu Asn Glu Leu Pro Pro Glu Asn Ile Glu Val Ser Val Gln  
225 230 235 240

Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr  
245 250 255

Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn  
260 265 270

His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr  
275 280 285

Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu  
290 295 300

Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu  
305 310 315 320

Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val  
325 330 335

Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala  
340 345 350

Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile  
355 360 365

Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile  
370 375 380

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cont.

Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn Leu Lys Pro Leu Thr  
385 390 395 400  
Val Tyr Cys Val Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn  
405 410 415  
Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly  
420 425 430  
Asn Thr Ser Lys  
435

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1755 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 27..1697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTGCAGGGAT CTGCGGCGGC TCCCAG ATG ATG GTC GTC CTC CTG GGC GCG ACG 53  
 Met Met Val Val Leu Leu Gly Ala Thr  
 1 5  
 ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA 101  
 Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala  
 10 15 20 25  
 GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTA GAG GTC GAC ATC ATA 149  
 Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile  
 30 35 40  
 GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG 197  
 Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly  
 45 50 55  
 AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG 245  
 Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp  
 60 65 70  
 ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT 293  
 Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe  
 75 80 85  
 TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA 341  
 Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg  
 90 95 100 105  
 GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA 389  
 Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr  
 110 115 120  
 CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT 437  
 Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala  
 125 130 135

C' cont.

GAA Glu	GAT Asp	AAG Lys 140	GCA Ala	ATA Ile	GTG Val	ATA Ile	CAC His 145	ATC Ile	TCT Ser	CCT Pro	GGA Gly	ACA Thr 150	AAA Lys	GAT Asp	AGT Ser	485
GTT Val	ATG Met 155	TGG Trp	GCT Ala	TTG Leu	GAT Asp	GGT Gly 160	TTA Leu	AGC Ser	TTT Phe	ACA Thr	TAT Tyr 165	AGC Ser	TTA Leu	CTT Leu	ATC Ile	533
TGG Trp 170	AAA Lys	AAC Asn	TCT Ser	TCA Ser	GGT Gly 175	GTA Val	GAA Glu	GAA Glu	AGG Arg	ATT Ile 180	GAA Glu	AAT Asn	ATT Ile	TAT Tyr	TCC Ser 185	581
AGA Arg	CAT His	AAA Lys	ATT Ile	TAT Tyr 190	AAA Lys	CTC Leu	TCA Ser	CCA Pro	GAG Glu 195	ACT Thr	ACT Thr	TAT Tyr	TGT Cys	CTA Leu 200	AAA Lys	629
GTT Val	AAA Lys	GCA Ala 205	GCA Ala	CTA Leu	CTT Leu	ACG Thr	TCA Ser	TGG Trp 210	AAA Lys	ATT Ile	GGT Gly	GTC Val	TAT Tyr 215	AGT Ser	CCA Pro	677
GTA Val	CAT His	TGT Cys 220	ATA Ile	AAG Lys	ACC Thr	ACA Thr	GTT Val 225	GAA Glu	AAT Asn	GAA Glu	CTA Leu	CCT Pro 230	CCA Pro	CCA Pro	GAA Glu	725
AAT Asn 235	ATA Ile	GAA Glu	GTC Val	AGT Ser	GTC Val	CAA Gln 240	AAT Asn	CAG Gln	AAC Asn	TAT Tyr	GTT Val 245	CTT Leu	AAA Lys	TGG Trp	GAT Asp	773
TAT Tyr 250	ACA Thr	TAT Tyr	GCA Ala	AAC Asn	ATG Met 255	ACC Thr	TTT Phe	CAA Gln	GTT Val	CAG Gln	TGG Trp 260	CTC Leu	CAC His	GCC Ala	TTT Phe 265	821
TTA Leu	AAA Lys	AGG Arg	AAT Asn	CCT Pro 270	GGA Gly	AAC Asn	CAT His	TTG Leu	TAT Tyr 275	AAA Lys	TGG Trp	AAA Lys	CAA Gln	ATA Ile 280	CCT Pro	869
GAC Asp	TGT Cys	GAA Glu	AAT Asn 285	GTC Val	AAA Lys	ACT Thr	ACC Thr	CAG Gln 290	TGT Cys	GTC Val	TTT Phe	CCT Pro	CAA Gln 295	AAC Asn	GTT Val	917
TTC Phe	CAA Gln 300	AAA Lys	GGA Gly	ATT Ile	TAC Tyr	CTT Leu	CTC Leu	CGC Arg 305	GTA Val	CAA Gln	GCA Ala	TCT Ser 310	GAT Asp	GGA Gly	AAT Asn	965
AAC Asn 315	ACA Thr	TCT Ser	TTT Phe	TGG Trp	TCT Ser	GAA Glu 320	GAG Glu	ATA Ile	AAG Lys	TTT Phe	GAT Asp 325	ACT Thr	GAA Glu	ATA Ile	CAA Gln	1013
GCT Ala 330	TTC Phe	CTA Leu	CTT Leu	CCT Pro	CCA Pro 335	GTC Val	TTT Phe	AAC Asn	ATT Ile	AGA Arg 340	TCC Ser	CTT Leu	AGT Ser	GAT Asp 345	TCA Ser	1061
TTC Phe	CAT His	ATC Ile	TAT Tyr	ATC Ile 350	GGT Gly	GCT Ala	CCA Pro	AAA Lys	CAG Gln 355	TCT Ser	GGA Gly	AAC Asn	ACG Thr	CCT Pro 360	GTG Val	1109
ATC Ile	CAG Gln	GAT Asp	TAT Tyr 365	CCA Pro	CTG Leu	ATT Ile	TAT Tyr	GAA Glu 370	ATT Ile	ATT Ile	TTT Phe	TGG Trp	GAA Glu 375	AAC Asn	ACT Thr	1157
TCA Ser	AAT Asn 380	GCT Ala	GAG Glu	AGA Arg	AAA Lys	ATT Ile	ATC Ile 385	GAG Glu	AAA Lys	AAA Lys	ACT Thr	GAT Asp 390	GTT Val	ACA Thr	GTT Val	1205
CCT Pro 395	AAT Asn	TTG Leu	AAA Lys	CCA Pro	CTG Leu	ACT Thr 400	GTA Val	TAT Tyr	TGT Cys	GTG Val	AAA Lys 405	GCC Ala	AGA Arg	GCA Ala	CAC His	1253

C  
cont.

ACC ATG GAT GAA AAG CTG AAT AAA AGC AGT GTT TTT AGT GAC GCT GTA 1301  
 Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val  
 410 415 420 425

TGT GAG AAA ACA AAA CCA GGA AAT ACC TCT AAA ATT TGG CTT ATA GTT 1349  
 Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp Leu Ile Val  
 430 435 440

GGA ATT TGT ATT GCA TTA TTT GCT CTC CCG TTT GTC ATT TAT GCT GCG 1397  
 Gly Ile Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile Tyr Ala Ala  
 445 450 455

AAA GTC TTC TTG AGA TGC ATC AAT TAT GTC TTC TTT CCA TCA CTT AAA 1445  
 Lys Val Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro Ser Leu Lys  
 460 465 470

CCT TCT TCC AGT ATA GAT GAG TAT TTC TCT GAA CAG CCA TTG AAG AAT 1493  
 Pro Ser Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro Leu Lys Asn  
 475 480 485

CTT CTG CTT TCA ACT TCT GAG GAA CAA ATC GAA AAA TGT TTC ATA ATT 1541  
 Leu Leu Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys Phe Ile Ile  
 490 495 500 505

GAA AAT ATA AGC ACA ATT GCT ACA GTA GAA GAA ACT AAT CAA ACT GAT 1589  
 Glu Asn Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn Gln Thr Asp  
 510 515 520

GAA GAT CAT AAA AAA TAC AGT TCC CAA ACT AGC CAA GAT TCA GGA AAT 1637  
 Glu Asp His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp Ser Gly Asn  
 525 530 535

TAT TCT AAT GAA GAT GAA AGC GAA AGT AAA ACA AGT GAA GAA CTA CAG 1685  
 Tyr Ser Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu Glu Leu Gln  
 540 545 550

CAG GAC TTT GTA TGACCAGAAA TGAAGTGTGT CAAGTATAAG GTTTTTTCAGC 1737  
 Gln Asp Phe Val  
 555

AGGAGTTACA CTGGTACC 1755

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 557 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val  
 1 5 10 15

Gly Pro Trp Val Leu Ser Ala Ala Ala Gly Gly Lys Asn Leu Lys Ser  
 20 25 30

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg  
 35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp  
 50 55 60

Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln  
 65 70 75 80  
 Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val  
 85 90 95  
 Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser  
 100 105 110  
 Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile  
 115 120 125  
 Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp Lys Ala Ile Val Ile  
 130 135 140  
 His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly  
 145 150 155 160  
 Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val  
 165 170 175  
 Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu  
 180 185 190  
 Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr  
 195 200 205  
 Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr  
 210 215 220  
 Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile Glu Val Ser Val Gln  
 225 230 235 240  
 Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr  
 245 250 255  
 Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn  
 260 265 270  
 His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr  
 275 280 285  
 Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu  
 290 295 300  
 Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu  
 305 310 315 320  
 Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val  
 325 330 335  
 Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala  
 340 345 350  
 Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile  
 355 360 365  
 Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile  
 370 375 380  
 Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn Leu Lys Pro Leu Thr  
 385 390 395 400  
 Val Tyr Cys Val Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn  
 405 410 415

C!  
 cont.



Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly  
420 425 430  
Asn Thr Ser Lys Ile Trp Leu Ile Val Gly Ile Cys Ile Ala Leu Phe  
435 440 445  
Ala Leu Pro Phe Val Ile Tyr Ala Ala Lys Val Phe Leu Arg Cys Ile  
450 455 460  
Asn Tyr Val Phe Phe Pro Ser Leu Lys Pro Ser Ser Ser Ile Asp Glu  
465 470 475 480  
Tyr Phe Ser Glu Gln Pro Leu Lys Asn Leu Leu Leu Ser Thr Ser Glu  
485 490 495  
Glu Gln Ile Glu Lys Cys Phe Ile Ile Glu Asn Ile Ser Thr Ile Ala  
500 505 510  
Thr Val Glu Glu Thr Asn Gln Thr Asp Glu Asp His Lys Lys Tyr Ser  
515 520 525  
Ser Gln Thr Ser Gln Asp Ser Gly Asn Tyr Ser Asn Glu Asp Glu Ser  
530 535 540  
Glu Ser Lys Thr Ser Glu Glu Leu Gln Gln Asp Phe Val  
545 550 555

C'  
corel